



1600

RAW SEQUENCE LISTING

DATE: 06/19/2003

PATENT APPLICATION: US/09/654,499

TIME: 16:02:29

Input Set : A:\4085-226-27.ST25.txt

Output Set: N:\CRF4\06192003\I654499.raw

3 <110> APPLICANT: Palmer, Michelle A.J.
 4 Gee, Melissa
 5 Tillotson, Bonnie
 6 Chang, Xiao-Jia
 8 <120> TITLE OF INVENTION: Receptor Function Assay for G-Protein Coupled Receptors and Orphan

9 Receptors by Reporter Enzyme Mutant Complementation
 11 <130> FILE REFERENCE: 4085-226-27
 13 <140> CURRENT APPLICATION NUMBER: US 09/654,499
 14 <141> CURRENT FILING DATE: 2000-09-01
 16 <150> PRIOR APPLICATION NUMBER: US 60/180,669
 17 <151> PRIOR FILING DATE: 2000-02-07
 19 <160> NUMBER OF SEQ ID NOS: 6
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 6700
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Nucleotide sequence for pICAST ALC
 W--> 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1457)...(4486)

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 37 tcctgccccg gctcagggcc agaacagat ggtccccaga tgcgggtccag ccctcagcag 180
 38 tttctagaga accatcagat gtttccaggg tgccccagg acctgaaatg accctgtgcc 240
 39 ttatttgaac taaccaatca gttcgtctct cgtttctgtt cgcgcgttc tgctccccga 300
 40 gctcaataaa agagcccaca acccctcact cggggcgcca gtctctccgat tgactgagtc 360
 41 gcccgggtac cgtgttatcc aataaacctt cttgcagttg catccgactt gtggtctcgc 420
 42 tgttctcttg gaggggtctc tctgagtgat tgactaccg tcagcggggg tctttcattt 480
 43 gggggctcgt ccgggatcgg gagaccctg ccaggggacc accgaccac caccgggagg 540
 44 caagctggcc agcaacttat ctgtgtctgt ccgattgtct agtgtctatg actgatttta 600
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 46 ctgacgagtt ctgaacaccc ggccgcaacc ctgggagacg tcccagggaac tttggggggc 720
 47 gtttttctgg ccgacctga ggaagggagt cgtgttgaa tccgaccgcg tcaggatatg 780
 48 tggttctggt aggagacgag aacctaaaac agttcccgcc tccgtctgaa tttttgcttt 840
 49 cggtttgaa ccgaagccgc gcgtcttgct tgctgcagca tcgttctgtg ttgtctctgt 900
 50 ctgactgtgt ttctgtattt gtctgaaaat tagggccaga ctgttaccac tcccttaagt 960
 51 ttgaccttag gtaactggaa agatgtcgag cggctcgctc acaaccagtc ggtagatgtc 1020
 52 aagaagagac gttgggttac cttctgctct gcagaatggc caacctttaa cgtcggatgg 1080
 53 ccgcgagacg gcacctttaa ccgagacctc atcaccagg ttaagatcaa ggtcttttca 1140
 54 cctggccgcg atggacaccc agaccaggtc cctacatcg tgacctggga agccttggt 1200
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58 atagggcgat tcgaatcagg ccttggcgcg ccggatcctt aattaagcgc aattgggagg 1440
59 tggcggtagc ctcgag atg ggc gtg att acg gat tca ctg gcc gtc gtg gcc 1492
60      Met Gly Val Ile Thr Asp Ser Leu Ala Val Val Ala
61      1      5      10
63 cgc acc gat cgc cct tcc caa cag tta cgc agc ctg aat ggc gaa tgg 1540
64 Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp
65      15      20      25
67 cgc ttt gcc tgg ttt ccg gca cca gaa gcg gtg ccg gaa agc tgg ctg 1588
68 Arg Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu
69      30      35      40
71 gag tgc gat ctt cct gag gcc gat act gtc gtc gtc ccc tca aac tgg 1636
72 Glu Cys Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp
73 45      50      55      60
75 cag atg cac ggt tac gat gcg ccc atc tac acc aac gtg acc tat ccc 1684
76 Gln Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro
77      65      70      75
79 att acg gtc aat ccg ccg ttt gtt ccc acg gag aat ccg acg ggt tgt 1732
80 Ile Thr Val Asn Pro Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys
81      80      85      90
83 tac tcg ctc aca ttt aat gtt gat gaa agc tgg cta cag gaa ggc cag 1780
84 Tyr Ser Leu Thr Phe Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln
85      95      100      105
87 acg cga att att ttt gat ggc gtt aac tcg gcg ttt cat ctg tgg tgc 1828
88 Thr Arg Ile Ile Phe Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys
89      110      115      120
91 aac ggg cgc tgg gtc ggt tac ggc cag gac agt cgt ttg ccg tct gaa 1876
92 Asn Gly Arg Trp Val Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu
93 125      130      135      140
95 ttt gac ctg agc gca ttt tta cgc gcc gga gaa aac cgc ctc gcg gtg 1924
96 Phe Asp Leu Ser Ala Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val
97      145      150      155
99 atg gtg ctg cgc tgg agt gac ggc agt tat ctg gaa gat cag gat atg 1972
100 Met Val Leu Arg Trp Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met
101      160      165      170
103 tgg cgg atg agc ggc att ttc cgt gac gtc tog ttg ctg cat aaa ccg 2020
104 Trp Arg Met Ser Gly Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro
105      175      180      185
107 act aca caa atc agc gat ttc cat gtt gcc act cgc ttt aat gat gat 2068
108 Thr Thr Gln Ile Ser Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp
109      190      195      200
111 ttc agc cgc gct gta ctg gag gct gaa gtt cag atg tgc ggc gag ttg 2116
112 Phe Ser Arg Ala Val Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu
113 205      210      215      220
115 cgt gac tac cta cgg gta aca gtt tct tta tgg cag ggt gaa acg cag 2164
116 Arg Asp Tyr Leu Arg Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln
117      225      230      235
119 gtc gcc agc ggc acc gcg cct ttc ggc ggt gaa att atc gat gag cgt 2212

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123	ggt	ggt	tat	gcc	gat	cgc	gtc	aca	cta	cgt	ctg	aac	gtc	gaa	aac	ccg	2260
124	Gly	Gly	Tyr	Ala	Asp	Arg	Val	Thr	Leu	Arg	Leu	Asn	Val	Glu	Asn	Pro	
125			255					260					265				
127	aaa	ctg	tgg	agc	gcc	gaa	atc	ccg	aat	ctc	tat	cgt	gcg	gtg	gtt	gaa	2308
128	Lys	Leu	Trp	Ser	Ala	Glu	Ile	Pro	Asn	Leu	Tyr	Arg	Ala	Val	Val	Glu	
129			270					275					280				
131	ctg	cac	acc	gcc	gac	ggc	acg	ctg	att	gaa	gca	gaa	gcc	tgc	gat	gtc	2356
132	Leu	His	Thr	Ala	Asp	Gly	Thr	Leu	Ile	Glu	Ala	Glu	Ala	Cys	Asp	Val	
133	285					290				295						300	
135	ggt	ttc	cgc	gag	gtg	cgg	att	gaa	aat	ggt	ctg	ctg	ctg	ctg	aac	ggc	2404
136	Gly	Phe	Arg	Glu	Val	Arg	Ile	Glu	Asn	Gly	Leu	Leu	Leu	Leu	Asn	Gly	
137				305					310					315			
139	aag	ccg	ttg	ctg	att	cga	ggc	gtt	aac	cgt	cac	gag	cat	cat	cct	ctg	2452
140	Lys	Pro	Leu	Leu	Ile	Arg	Gly	Val	Asn	Arg	His	Glu	His	His	Pro	Leu	
141				320					325					330			
143	cat	ggt	cag	gtc	atg	gat	gag	cag	acg	atg	gtg	cag	gat	atc	ctg	ctg	2500
144	His	Gly	Gln	Val	Met	Asp	Glu	Gln	Thr	Met	Val	Gln	Asp	Ile	Leu	Leu	
145			335					340					345				
147	atg	aag	cag	aac	aac	ttt	aac	gcc	gtg	cgc	tgt	tcg	cat	tat	ccg	aac	2548
148	Met	Lys	Gln	Asn	Asn	Phe	Asn	Ala	Val	Arg	Cys	Ser	His	Tyr	Pro	Asn	
149			350				355					360					
151	cat	ccg	ctg	tgg	tac	acg	ctg	tgc	gac	cgc	tac	ggc	ctg	tat	gtg	gtg	2596
152	His	Pro	Leu	Trp	Tyr	Thr	Leu	Cys	Asp	Arg	Tyr	Gly	Leu	Tyr	Val	Val	
153	365					370				375						380	
155	gat	gaa	gcc	aat	att	gaa	acc	cac	ggc	atg	gtg	cca	atg	aat	cgt	ctg	2644
156	Asp	Glu	Ala	Asn	Ile	Glu	Thr	His	Gly	Met	Val	Pro	Met	Asn	Arg	Leu	
157				385					390					395			
159	acc	gat	gat	ccg	cgc	tgg	cta	ccg	gcg	atg	agc	gaa	cgc	gta	acg	cga	2692
160	Thr	Asp	Asp	Pro	Arg	Trp	Leu	Pro	Ala	Met	Ser	Glu	Arg	Val	Thr	Arg	
161				400					405					410			
163	atg	gtg	cag	cgc	gat	cgt	aat	cac	ccg	agt	gtg	atc	atc	tgg	tcg	ctg	2740
164	Met	Val	Gln	Arg	Asp	Arg	Asn	His	Pro	Ser	Val	Ile	Ile	Trp	Ser	Leu	
165			415				420						425				
167	ggg	aat	gaa	tca	ggc	cac	ggc	gct	aat	cac	gac	gcg	ctg	tat	cgc	tgg	2788
168	Gly	Asn	Glu	Ser	Gly	His	Gly	Ala	Asn	His	Asp	Ala	Leu	Tyr	Arg	Trp	
169		430					435					440					
171	atc	aaa	tct	gtc	gat	cct	tcc	cgc	ccg	gtg	cag	tat	gaa	ggc	ggc	gga	2836
172	Ile	Lys	Ser	Val	Asp	Pro	Ser	Arg	Pro	Val	Gln	Tyr	Glu	Gly	Gly	Gly	
173	445					450				455						460	
175	gcc	gac	acc	acg	gcc	acc	gat	att	att	tgc	ccg	atg	tac	gcg	cgc	gtg	2884
176	Ala	Asp	Thr	Thr	Ala	Thr	Asp	Ile	Ile	Cys	Pro	Met	Tyr	Ala	Arg	Val	
177				465					470					475			
179	gat	gaa	gac	cag	ccc	ttc	ccg	gct	gtg	ccg	aaa	tgg	tcc	atc	aaa	aaa	2932
180	Asp	Glu	Asp	Gln	Pro	Phe	Pro	Ala	Val	Pro	Lys	Trp	Ser	Ile	Lys	Lys	
181			480					485					490				
183	tgg	ctt	tcg	cta	cct	gga	gag	acg	cgc	ccg	ctg	atc	ctt	tgc	gaa	tac	2980
184	Trp	Leu	Ser	Leu	Pro	Gly	Glu	Thr	Arg	Pro	Leu	Ile	Leu	Cys	Glu	Tyr	

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189 510 515 520				
191 gcg ttt cgt cag tat ccc cgt tta cag ggc ggc ttc gtc tgg gac tgg	3076			
192 Ala Phe Arg Gln Tyr Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Trp				
193 525 530 535 540				
195 gtg gat cag tcg ctg att aaa tat gat gaa aac ggc aac ccg tgg tcg	3124			
196 Val Asp Gln Ser Leu Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser				
197 545 550 555				
199 gct tac ggc ggt gat ttt ggc gat acg ccg aac gat cgc cag ttc tgt	3172			
200 Ala Tyr Gly Gly Asp Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys				
201 560 565 570				
203 atg aac ggt ctg gtc ttt gcc gac cgc acg ccg cat cca gcg ctg acg	3220			
204 Met Asn Gly Leu Val Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr				
205 575 580 585				
207 gaa gca aaa cac cag cag cag ttt ttc cag ttc cgt tta tcc ggg caa	3268			
208 Glu Ala Lys His Gln Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln				
209 590 595 600				
211 acc atc gaa gtg acc agc gaa tac ctg ttc cgt cat agc gat aac gag	3316			
212 Thr Ile Glu Val Thr Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu				
213 605 610 615 620				
215 ctc ctg cac tgg atg gtg gcg ctg gat ggt aag ccg ctg gca agc ggt	3364			
216 Leu Leu His Trp Met Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly				
217 625 630 635				
219 gaa gtg cct ctg gat gtc gct cca caa ggt aaa cag ttg att gaa ctg	3412			
220 Glu Val Pro Leu Asp Val Ala Pro Gln Gly Lys Gln Leu Ile Glu Leu				
221 640 645 650				
223 cct gaa cta ccg cag ccg gag agc gcc ggg caa ctc tgg ctc aca gta	3460			
224 Pro Glu Leu Pro Gln Pro Glu Ser Ala Gly Gln Leu Trp Leu Thr Val				
225 655 660 665				
227 cgc gta gtg caa ccg aac gcg acc gca tgg tca gaa gcc ggg cac atc	3508			
228 Arg Val Val Gln Pro Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile				
229 670 675 680				
231 agc gcc tgg cag cag tgg cgt ctg gcg gaa aac ctc agt gtg acg ctc	3556			
232 Ser Ala Trp Gln Gln Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu				
233 685 690 695 700				
235 ccc gcc gcg tcc cac gcc atc ccg cat ctg acc acc agc gaa atg gat	3604			
236 Pro Ala Ala Ser His Ala Ile Pro His Leu Thr Thr Ser Glu Met Asp				
237 705 710 715				
239 ttt tgc atc gag ctg ggt aat aag cgt tgg caa ttt aac cgc cag tca	3652			
240 Phe Cys Ile Glu Leu Gly Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser				
241 720 725 730				
243 ggc ttt ctt tca cag atg tgg att ggc gat aaa aaa caa ctg ctg acg	3700			
244 Gly Phe Leu Ser Gln Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr				
245 735 740 745				
247 ccg ctg cgc gat cag ttc acc cgt gca ccg ctg gat aac gac att ggc	3748			
248 Pro Leu Arg Asp Gln Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly				
249 750 755 760				

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251 gta agt gaa gcg acc cgc att gac cct aac gcc tgg gtc gaa cgc tgg 3796
252 Val Ser Glu Ala Thr Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp
253 765 770 775 780
255 aag gcg gcg ggc cat tac cag gcc gaa gca gcg ttg ttg cag tgc acg 3844
256 Lys Ala Ala Gly His Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr
257 785 790 795
259 gca gat aca ctt gct gat gcg gtg ctg att acg acc gct cac gcg tgg 3892
260 Ala Asp Thr Leu Ala Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp
261 800 805 810
263 cag cat cag ggg aaa acc tta ttt atc agc cgg aaa acc tac cgg att 3940
264 Gln His Gln Gly Lys Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile
265 815 820 825
267 gat ggt agt ggt caa atg gcg att acc gtt gat gtt gaa gtg gcg agc 3988
268 Asp Gly Ser Gly Gln Met Ala Ile Thr Val Asp Val Glu Val Ala Ser
269 830 835 840
271 gat aca ccg cat ccg gcg cgg att ggc ctg aac tgc cag ctg gcg cag 4036
272 Asp Thr Pro His Pro Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln
273 845 850 855 860
275 gta gca gag cgg gta aac tgg ctc gga tta ggg ccg caa gaa aac tat 4084
276 Val Ala Glu Arg Val Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr
277 865 870 875
279 ccc gac cgc ctt act gcc gcc tgt ttt gac cgc tgg gat ctg cca ttg 4132
280 Pro Asp Arg Leu Thr Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu
281 880 885 890
283 tca gac atg tat acc ccg tac gtc ttc ccg agc gaa aac ggt ctg cgc 4180
284 Ser Asp Met Tyr Thr Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg
285 895 900 905
287 tgc ggg acg cgc gaa ttg aat tat ggc cca cac cag tgg cgc ggc gac 4228
288 Cys Gly Thr Arg Glu Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp
289 910 915 920
291 ttc cag ttc aac atc agc cgc tac agt caa cag caa ctg atg gaa acc 4276
292 Phe Gln Phe Asn Ile Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr
293 925 930 935 940
295 agc cat cgc cat ctg ctg cac gcg gaa gaa ggc aca tgg ctg aat atc 4324
296 Ser His Arg His Leu Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile
297 945 950 955
299 gac ggt ttc cat atg ggg att ggt ggc gac gac tcc tgg agc ccg tca 4372
300 Asp Gly Phe His Met Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser
301 960 965 970
303 gta tcg gcg gaa ttc cag ctg agc gcc ggt cgc tac cat tac cag ttg 4420
304 Val Ser Ala Glu Phe Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu
305 975 980 985
307 gtc tgg tgt caa aaa aga tct gac tat aaa gat gag gac ctc gac cat 4468
308 Val Trp Cys Gln Lys Arg Ser Asp Tyr Lys Asp Glu Asp Leu Asp His
309 990 995 1000
311 cat cat cat cat cac cgg taataatagg tagataagtg actgattaga 4516
312 His His His His His Arg
313 1005 1010
315 tgcattgatac cctcgaccaa ttccggttat ttccaccat attgccgtct tttggcaatg 4576

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VERIFICATION SUMMARY

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L:31 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!

L:34 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1